Department of Microbiology and Plant Pathology, Tree Protection Co-operative Programme (TPCP), Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa

Fungi residing in the *Cryphonectriaceae* include some of the world's most important tree pathogens. These include *Cryphonectria parasitica* that causes chestnut blight in North America and Europe and *Chrysoporthe* spp. that are important canker pathogens of trees such as *Eucalyptus* spp. in South Africa, South America and Asia. Currently, four species of *Cryphonectriaceae* are known from Africa namely *Chrysoporthe austroafricana, Chr. cubensis*, *Celoporthe dispersa*, and *Holocryphia eucalypti*. These species infect trees in three families in the order Myrtales namely *Myrtaceae*, *Melastomataceae* and *Heteropyxidaceae*. Studies conducted on these pathogens have produced good evidence to suggest that *Chr. cubensis* and *H. eucalypti* are introduced pathogens, while *Chr. austroafricana* is native to Africa. Much, however, remains unknown regarding the origins and impact of the Cryphonectriaceae in Africa and regular surveys are being conducted to increase this base of knowledge. During the past year surveys in Cameroon and South Africa yielded fruiting structures resembling those of the *Cryphonectriaceae* on *Terminalia ivorensis* and *Terminalia mantaly* (*Combretaceae*) in Cameroon and *Galpinia transvaalica* (*Lythraceae*) in South Africa. These fungi were identified based on morphology and DNA sequence comparisons which showed that they represent a previously undescribed genus in the Cryphonectriaceae. DNA sequence data further showed that the fungus collected from *G. transvaalica* in South Africa represent a distinct species from that collected in Cameroon. This is only the second record of a member of the *Cryphonectriaceae* infecting *Combretaceae* in Africa and isolates from South Africa represent the first record of the *Cryphonectriaceae* infecting the *Lythraceae* in Africa. The origin and impact of these two species on their native hosts are not yet clear, although the fungus from *G. transvaalica* was collected from stem cankers resulting in branch die-back on these trees. More extensive surveys are underway to investigate this further.

doi:10.1016/j.sajb.2009.02.121

A multidisciplinary study of indigenous aromatic plants

A.M. Viljoen
Department of Pharmaceutical Sciences, Tshwane University of Technology, Private Bag X680, Pretoria 0001, South Africa

South Africa has offered the world two indigenous aromatic plants which have both been developed into a commercial success. Geranium oil (obtained from various cultivars of *Pelargonium graveolens*) and Buchu oil (from *Agathosma betulina*) are only two species out of the near 700 aromatic plants indigenous to South Africa. It remains ironic that most of the other aromatic species have until recently been neglected, with little research being carried out to explore their possible future use and application in consumer products. Most often, aromatic plants are studied either to: 1) determine the chemical composition of the oil; 2) search for interesting chemotypes, 3) investigate the biological activity (especially for plants used in African traditional healing), 4) to resolve or confirm a taxonomic placement. Generally these aspects are undertaken independently. In 1999 an ambitious project was initiated to record the essential oil composition and biological activities of South Africa's extra-special botanical resources. Using a classical multidisciplinary approach results obtained for some of the most abundant indigenous aromatic genera (e.g. *Salvia*, *Lippa*, *Eriocephalus*, *Agathosma*, *Pelargonium*) will be discussed in terms of results obtained for aspects 1-4 mentioned above. The paper is a brief reflection of past and present research.

doi:10.1016/j.sajb.2009.02.122

Understanding plant cystatin structure/function relationships through homology modeling

B.J. Vorster[a], Ö. Tastan Bishop[b], U. Schlüter[a], K. Kunert[a], D. Michaud[c]
[a]*Department of Plant Science, University of Pretoria, Pretoria 0002, South Africa*
[b]*Bioinformatics and Computational Biology Unit, Department of Biochemistry, University of Pretoria, Pretoria 0002, South Africa*
[c]*Département de Phytologie, Université Laval, Quebec City (QC), Canada G1V 0A6*

In plants, protease inhibitors of the cystatin superfamily regulate cysteine proteinases in several important physiological and cellular processes, including organogenesis, storage protein turnover, programmed cell death, tolerance to abiotic stresses, and defence against herbivorous predators and pathogens. Cystatins form tight, reversible complexes with cysteine proteinases, acting as pseudo-substrates that enter the active site cleft of target enzymes. Recent studies have shown that proteins involved in host defence responses are subject to adaptive evolution [or positive selection], as a result of differential selection pressures on amino acid sites interacting with the target molecules of invading or predatory organisms. Based on these findings, amino acid substitutions at positively selected sites were performed on a model cystatin from tomato, and shown to modulate the inhibitory potency of this inhibitor against various cysteine proteinases. Here we are using a homology modeling approach to investigate structure/function relationships between the same mutant cystatins and various cysteine proteinases, with the aim of better understanding their mode of action at the molecular level and facilitating the identification of potentially relevant mutations for cystatin improvement in a biotechnological context.

doi:10.1016/j.sajb.2009.02.123